

Amendments to the Specification:

Please insert the Sequence Listing, attached hereto, after the claims, as page 1.

Please replace the paragraph at page 20, lines 16-31, with the following amended paragraph:

As indicated above, a sequence-activity model used with the present invention relates protein sequence information to protein activity. The protein sequence information used by the model may take many forms. Frequently, it is a complete sequence of the amino acid residues in a protein; e.g., HGPVFSTGGA (SEQ ID NO: 1). . . . In some cases, however, it may be unnecessary to provide the complete amino acid sequence. For example, it may be sufficient to provide only those residues that are to be varied in a particular research effort. At later stages in research, for example, many residues may be fixed and only limited regions of sequence space remain to be explored. In such situations, it may be convenient to provide sequence activity models that require, as inputs, only the identification of those residues in the regions of the protein where the exploration continues. Still further, some models may not require exact identities of residues at the residue positions, but instead identify one or more physical or chemical properties that characterize the amino acid at a particular residue position. For example, the model may require specification of residue positions by bulk, hydrophobicity, acidity, etc. In some models, combinations of such properties are employed.